

**Amendments to the Claims:**

Claims 20, 24-26, 29, 30, 33, 35-39, and 42-47 are amended herein. Claims 34 and 41 are canceled herein. This listing of claims will replace all prior versions, and listings, of claims in the application.

**Listing of Claims:**

Claims 1 -19. (previously canceled)

Claim 20. (currently amended) A method for analyzing a nucleic acid sample comprising:

fragmenting the nucleic acid sample using a first and a second restriction enzyme to produce fragments;

ligating a first and a second adaptor adapters to the fragments, wherein the first adaptor is blocked from ligation to the fragments at the 3' end of one strand of the first adaptor, and the second adaptor is blocked from ligation to the fragments at the 5' end of one strand of the second adaptor and wherein the first adaptor ligates to fragments cut by the first restriction enzyme and the second adaptor ligates to fragments cut by the second restriction enzyme;

amplifying the fragments, wherein the fragments that are were cut on one end by the first restriction enzyme and on the other end by the second restriction enzyme and are ligated to both the first adaptor and the second adaptor are enriched in the amplification product relative to the fragments that are were cut on both ends by the first restriction enzyme, and to the fragments that are cut on both ends by the second restriction enzyme the same restriction enzyme;

providing a nucleic acid array consisting essentially of probes designed to detect the alleles sequence present at a plurality of polymorphisms predicted to be present on in the fragments that are were cut on one end by the first restriction enzyme and on the other end by the second restriction enzyme;

hybridizing the amplified fragments to the array; and

analyzing a hybridization pattern resulting from the hybridization.

Claim 21. (canceled)

Claim 22. (currently amended) The method of claim 20 wherein the polymorphisms are single nucleotide polymorphisms (SNPs).

Claim 23. (canceled)

Claim 24. (currently amended) The method of claim 20 wherein the polymorphisms predicted to be present ~~on~~ in the fragments that are ~~were~~ cut on one end by the first restriction enzyme and on the other end by the second restriction enzyme are first determined by a computer system.

Claim 25. (currently amended) A method of determining the alleles sequence present at a polymorphism in an individual comprising:

providing a nucleic acid sample from the individual;

fragmenting the nucleic acid sample using a first and a second restriction enzyme to produce fragments wherein the polymorphism is predicted to be on a fragment that is ~~was~~ cut on one end by the first restriction enzyme and on the other end by the second restriction enzyme;

ligating a first and a second adaptor adapters to the fragments, wherein the first adaptor is blocked from ligation to the fragments at the 3' end of one strand of the first adaptor, and the second adaptor is blocked from ligation to the fragments at the 5' end of one strand of the second adaptor and wherein the first adaptor ligates to fragments cut by the first restriction enzyme and the second adaptor ligates to fragments cut by the second restriction enzyme; and

amplifying the fragments, wherein the fragments that are ~~were~~ cut on one end by the first restriction enzyme and on the other end by the second restriction enzyme and are ligated to both the first adaptor and the second adaptor are enriched in the amplification product relative to the fragments that are ~~were~~ cut on both ends by the first restriction enzyme, and to the fragments that are cut on both ends by the second restriction enzyme ~~the same restriction enzyme~~;

providing a nucleic acid array consisting essentially of probes designed to detect the alleles present at sequence of a plurality of polymorphisms predicted to be present ~~on~~ in the fragments that are ~~were~~ cut on one end by the first restriction enzyme and on the other end by the second restriction enzyme;

hybridizing the amplified fragments to the array;  
generating a hybridization pattern resulting from the hybridization; and  
determining the ~~alleles~~ sequence present at the polymorphism in the individual based upon an analysis of the hybridization pattern.

Claim 26. (previously presented) The method of claim 25 wherein the polymorphism is a single nucleotide polymorphism (SNP).

Claim 27. (previously presented) The method of claim 26 wherein the SNP is associated with a disease.

Claim 28. (previously presented) The method of claim 26 wherein the SNP is associated with the efficacy of a drug.

Claim 29. (currently amended) A method of determining the ~~alleles~~ sequence present at a single nucleotide polymorphism in a population of individuals comprising:

providing a first nucleic acid sample from each of the individuals;

providing a second nucleic acid sample by:

fragmenting the first nucleic acid sample using a first and a second restriction enzyme to produce fragments wherein the polymorphism is predicted to be on a fragment that is was cut on one end by the first restriction enzyme and on the other end by the second restriction enzyme;

ligating a first and a second adaptor adapters to the fragments, wherein the first adaptor is blocked from ligation to the fragments at the 3' end of one strand of the first adaptor, and the second adaptor is blocked from ligation to the fragments at the 5' end of one strand of the second adaptor and wherein the first adaptor ligates to fragments cut by the first restriction enzyme and the second adaptor ligates to fragments cut by the second restriction enzyme; and

amplifying the fragments, wherein the fragments that ~~are~~ were cut on one end by the first restriction enzyme and on the other end by the second restriction enzyme and are ligated to both the first and the second adaptor are predominant in the amplification product relative to the fragments that ~~are~~ were cut on both ends by only the first restriction enzyme, and to the

fragments that are cut on both ends by only the second restriction enzyme the same restriction enzyme;

providing a plurality of identical nucleic acid arrays wherein the arrays consist essentially of probes to determine the alleles sequence present at a plurality of polymorphisms predicted to be present ~~on in the~~ fragments that are ~~were~~ cut on one end by the first restriction enzyme and on the other end by the second restriction enzyme;

hybridizing each of the second nucleic acid samples to one of the plurality of identical arrays;

generating a plurality of hybridization patterns resulting from the hybridizations; and  
analyzing the hybridization patterns to determine the alleles sequences present at the polymorphism in the population of individuals.

Claim 30. (previously presented) The method of claim 29 wherein the polymorphism is a single nucleotide polymorphism (SNP).

Claim 31. (previously presented) The method of claim 30 wherein the SNP is associated with a disease.

Claim 32. (previously presented) The method of claim 30 wherein the SNP is associated with the efficacy of a drug.

Claim 33. (currently amended) A method for genotyping an individual comprising:

providing a first nucleic sample from the individual;

providing a second nucleic acid sample by:

fragmenting the first nucleic acid sample using a first and a second restriction enzyme to produce fragments wherein a collection of polymorphisms is predicted to be present ~~on in the~~ fragments cut on one end by the first restriction enzyme and on the other end by the second restriction enzyme;

ligating a first and a second adaptor ~~adaptors~~ to the fragments wherein the first adaptor is blocked from ligation to the fragments at the 3' end of one strand of the first adaptor, and the second adaptor is blocked from ligation to the fragments at the 5' end of one strand of the second

adaptor and wherein the first adaptor ligates to fragments cut by the first restriction enzyme and the second adaptor ligates to fragments cut by the second restriction enzyme; and

amplifying the fragments, wherein the fragments that ~~are~~ were cut on one end by the first restriction enzyme and on the other end by the second restriction enzyme and are ligated to both the first and the second adaptor are predominant in the amplification product relative to the fragments that ~~are~~ were cut on both ends by only the first restriction enzyme, and to the fragments that are cut on both ends by only the second restriction enzyme the same restriction enzyme;

hybridizing the second nucleic acid sample to an array designed to determine the ~~presence or absence of one or more alleles of~~ sequences present at one or more polymorphisms present in the collection of polymorphisms;

generating a hybridization pattern resulting from the hybridizations; and

determining the ~~presence or absence of the one or more alleles of~~ sequences present at one or more polymorphisms present in the collection of polymorphisms.

Claim 34. (canceled)

Claim 35. (currently amended) The method of claim 20 wherein the fragments that are ~~were~~ cut on one end by the first restriction enzyme and on the other end by the second restriction enzyme comprise at least 0.01% of the ~~first~~ nucleic acid sample.

Claim 36. (currently amended) The method of claim 20 wherein the fragments that are ~~were~~ cut on one end by the first restriction enzyme and on the other end by the second restriction enzyme comprise at least 0.05% of the ~~first~~ nucleic acid sample.

Claim 37. (currently amended) The method of claim 20 wherein the fragments that are ~~were~~ cut on one end by the first restriction enzyme and on the other end by the second restriction enzyme comprise at least 3% of the ~~first~~ nucleic acid sample.

Claim 38. (currently amended) The method of claim 20 wherein the fragments that are were cut on one end by the first restriction enzyme and on the other end by the second restriction enzyme comprise at least 12% of the ~~first~~ nucleic acid sample.

Claim 39. (currently amended) The method of claim 20 wherein the fragments that are were cut on one end by the first restriction enzyme and on the other end by the second restriction enzyme comprise at least 30% of the ~~first~~ nucleic acid sample.

Claim 40. (previously presented) The method of claim 20 wherein the nucleic acid sample is genomic DNA, DNA, or double stranded cDNA derived from RNA, total RNA or mRNA.

Claim 41. (canceled)

Claim 42. (currently amended) The method of claim 20 ~~41~~ wherein ligation is blocked by introducing a gap of at least one nucleotide between one strand of the adaptor and one strand of the fragment.

Claim 43. (currently amended) The method of claim 20 ~~41~~ wherein ligation is blocked by the absence of a phosphate at the 5' end of an adaptor strand.

Claim 44. (currently amended) The method of claim 20 ~~41~~ wherein ligation is blocked by the presence of a modified nucleotide at the 5' or 3' end of an adaptor strand.

Claim 45. (currently amended) The method of claim 20 ~~41~~ wherein ligation is blocked by a terminal modification in one strand of an adaptor.

Claim 46. (currently amended) The method of claim 20 ~~41~~ wherein ligation is blocked at the 5' end of one strand of one adaptor and at the 3' end of one strand of the other adaptor.

Claim 47. (currently amended) The method of claim 20 ~~41~~ wherein ligation is blocked at the 5' end of both strands of one adaptor and at the 3' end of both strands of the other adaptor.